

SEQUENCE LISTING

<110> Rozzell, J. David
Bui, Peter
Hua, Ling

<120> SYNTHETIC GENES FOR ENHANCED EXPRESSION

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<150> 09/494,921

<151> 2000-01-31

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<170> PatentIn version 3.0

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15

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 <212> DNA
 <213> Saccharomyces cerevisiae

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 Lys Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Met
 100 105 110
 His Trp Pro Val Pro Leu Lys Thr Asp Arg Val Thr Asp Gly Asn Val
 115 120 125
 Leu Cys Ile Pro Thr Leu Glu Asp Gly Thr Val Asp Ile Asp Thr Lys
 130 135 140
 Glu Trp Asn Phe Ile Lys Thr Trp Glu Leu Met Gln Glu Leu Pro Lys
 145 150 155 160
 Thr Gly Lys Thr Lys Ala Val Gly Val Ser Asn Phe Ser Ile Asn Asn
 165 170 175
 Ile Lys Glu Leu Leu Glu Ser Pro Asn Asn Lys Val Val Pro Ala Thr
 180 185 190
 Asn Gln Ile Glu Ile His Pro Leu Leu Pro Gln Asp Glu Leu Ile Ala
 195 200 205
 Phe Cys Lys Glu Lys Gly Ile Val Val Glu Ala Tyr Ser Pro Phe Gly
 210 215 220
 Ser Ala Asn Ala Pro Leu Leu Lys Glu Gln Ala Ile Ile Asp Met Ala
 225 230 235 240
 Lys Lys His Gly Val Glu Pro Ala Gln Leu Ile Ile Ser Trp Ser Ile
 245 250 255
 Gln Arg Gly Tyr Val Val Leu Ala Lys Ser Val Asn Pro Glu Arg Ile
 260 265 270
 Val Ser Asn Phe Lys Ile Phe Thr Leu Pro Glu Asp Asp Phe Lys Thr
 275 280 285
 Ile Ser Asn Leu Ser Lys Val His Gly Thr Lys Arg Val Val Asp Met
 290 295 300
 Lys Trp Gly Ser Phe Pro Ile Phe Gln
 305 310

<210> 40

<211> 942

<212> DNA

<213> Artificial Sequence

<400> 40

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 atcgagcac tgaaagcagg ttaccgtcac atcgacgcag cagcaatcta cctgaacgaa 180
 gaagaagtag gtcgtgcaat caaagactcc ggtgttccgc gtgaagaaat ctttatcact 240
 actaaactgt ggggtactga acagcgtgac ccggaagcag cactgaacaa atctctgaaa 300

cgtctggggtc	tggactacgt	agacctgtac	ctgatgcact	ggccggtacc	gctgaaaact	360
gaccgtgttta	ctgatggtaa	cgttctgtgt	attccgactc	tggaagacgg	tactgtagac	420
atcgacacta	aggaatggaa	cttcatcaag	acttgggaac	tgatgcagga	actgccgaaa	480
actggtaaaa	ctaaagcagt	aggtgtttcc	aacttctcta	tcaacaacat	caaagaactg	540
ctggaatctc	cgaacaacaa	agtagtaccg	gcaactaacc	agatcgaaat	ccacccgctg	600
ctgccgcagg	acgaactgat	cgcattctgc	aaagagaaaag	gtatcgtagt	agaagcatac	660
tctccgttcg	gctctgcaaa	cgcaccgctg	ctgaaagaac	aggcaatcat	cgacatggca	720
aagaaacacg	gtgtagaacc	ggcacagctg	atcatctctt	ggctatatcca	gcgtgggttac	780
gtagtactgg	caaaatctgt	aaaccocggaa	cgtatcgtat	ctaacttcaa	aatcttcact	840
ctgccggaag	acgacttcaa	aactatctct	aacctgtcca	aagttcacgg	tactaaacgt	900
gtagtagaca	tgaaatgggg	ttctttcccg	atcttccagt	aa		942

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<210> 41
<211> 939
<212> DNA
<213> Saccharomyces cerevisiae
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<400>	41
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accgctttga aagatggcta ccgacacatt gatactgctg ctatttaccg taatgaagac	180
caagtcggtc aagccatcaa ggattcaggt gttcctcggg aagaaatctt tgttactaca	240
aagttatggt gtacacaaca ccacgaacct gaagtagcgc tggatcaatc actaaagagg	300
ttaggattgg actacgtaga cttatatattg atgcattggc ctgccagatt agatccagcc	360
tacatcaaaa atgaagacat cttgagtgtg ccaacaaaga aggatggttc tcgtgcagtg	420
gatatcacca attggaattt catcaaac acc tgggaattaa tgcaggaact accaaagact	480
ggtaaaaacta aggccgttg agtctccaac ttttctataa ataacctgaa agatctatta	540
gcattctcaag gtaataagct tacgccagct gctaaccaag tcgaaataca tccattacta	600
cctcaagacg aattgattaa tttttgtaa agtaaaggca ttgtggttga agcttatctt	660
ccgttaggta gtaccgatgc tccactattg aaggaaccgg ttatccttga aattgcgaag	720
aaaaataacg ttcaaccgg acacgttgtt attagctggc acgtccaaag aggttatgtt	780
gtcttgccaa aatctgtgaa tcccgatcga atcaaacga acaggaaaat atttactttg	840
tctactgagg actttgaagc tatcaataac atatcgaagg aaaagggcga aaaaaggggt	900
gtacatccaa attggtctcc ttctgaagta ttcaagtaa	939

275

280

285

Asn Asn Ile Ser Lys Glu Lys Gly Glu Lys Arg Val Val His Pro Asn
290 295 300

Trp Ser Pro Phe Glu Val Phe Lys
305 310

<210> 43
<211> 942
<212> DNA
<213> Artificial Sequence

<400> 43
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atcccgc aaa tcggcctggg tacttg gcaa tctaaagaaa acgacgcata caaggctggt 120
ctgactgctc tgaaggatgg ctatcgctcac attgatactg ctgctattta tcgtaacgag 180
gaccaggtag gtcaggcaat caaggactct ggcgttccgc gtgaggaaat cttcgtaact 240
accaaactgt ggtgcactca gcatcatgaa ccggaagtag cactggatca atctctgaag 300
cgtctgggtc tggactatgt tgatctgtac ctgatgcatt ggccggcgcg cctggacca 360
gcgtatatta aaaacgaaga tatcctgtct gttccgacta agaaagacgg ctctcgtgct 420
gttgacatca ctaactggaa cttcatcaag acctgggaac tgatgcagga actgccgaag 480
actggtaaaa ctaaagctgt tggcgtatct aacttctcca tcaacaacct gaaggacctg 540
ctggcatccc agggcaacaa gctgactccg gctgctaacc aagtagagat ccaccgctg 600
ctgccgcagg acgaactgat caacttctgt aaatctaaag gcattgtagt tgaagcatat 660
tctcgcgtgg gttctaccga tgcgccactg ctgaaagagc cggtaatcct ggagatcgcg 720
aagaaaaaca acgtacaacc aggtcatgta gtaatctctt ggcacgtaca gcgcggctac 780
gtagttctgc cgaagtctgt aaaccggat cgtatcaaaa ctaaccgtaa aatctttacc 840
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gtagttcacc caaactggtc cccgtttgaa gtattcaagt aa 942

<210> 44
<211> 313
<212> PRT
<213> Artificial Sequence

<400> 44

Met Gly Pro Ala Thr Leu His Asp Ser Thr Lys Ile Leu Ser Leu Asn
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Thr Gly Ala Gln Ile Pro Gln Ile Gly Leu Gly Thr Trp Gln Ser Lys
20 25 30

Glu Asn Asp Ala Tyr Lys Ala Val Leu Thr Ala Leu Lys Asp Gly Tyr

35					40					45					
Arg	His	Ile	Asp	Thr	Ala	Ala	Ile	Tyr	Arg	Asn	Glu	Asp	Gln	Val	Gly
50					55					60					
Gln	Ala	Ile	Lys	Asp	Ser	Gly	Val	Pro	Arg	Glu	Glu	Ile	Phe	Val	Thr
65					70					75					80
Thr	Lys	Leu	Trp	Cys	Thr	Gln	His	His	Glu	Pro	Glu	Val	Ala	Leu	Asp
				85					90					95	
Gln	Ser	Leu	Lys	Arg	Leu	Gly	Leu	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Met
			100					105					110		
His	Trp	Pro	Ala	Arg	Leu	Asp	Pro	Ala	Tyr	Ile	Lys	Asn	Glu	Asp	Ile
		115					120					125			
Leu	Ser	Val	Pro	Thr	Lys	Lys	Asp	Gly	Ser	Arg	Ala	Val	Asp	Ile	Thr
	130					135					140				
Asn	Trp	Asn	Phe	Ile	Lys	Thr	Trp	Glu	Leu	Met	Gln	Glu	Leu	Pro	Lys
145					150					155					160
Thr	Gly	Lys	Thr	Lys	Ala	Val	Gly	Val	Ser	Asn	Phe	Ser	Ile	Asn	Asn
				165					170					175	
Leu	Lys	Asp	Leu	Leu	Ala	Ser	Gln	Gly	Asn	Lys	Leu	Thr	Pro	Ala	Ala
			180					185					190		
Asn	Gln	Val	Glu	Ile	His	Pro	Leu	Leu	Pro	Gln	Asp	Glu	Leu	Ile	Asn
		195					200					205			
Phe	Cys	Lys	Ser	Lys	Gly	Ile	Val	Val	Glu	Ala	Tyr	Ser	Pro	Leu	Gly
	210					215					220				
Ser	Thr	Asp	Ala	Pro	Leu	Leu	Lys	Glu	Pro	Val	Ile	Leu	Glu	Ile	Ala
225					230					235					240
Lys	Lys	Asn	Asn	Val	Gln	Pro	Gly	His	Val	Val	Ile	Ser	Trp	His	Val
				245					250					255	
Gln	Arg	Gly	Tyr	Val	Val	Leu	Pro	Lys	Ser	Val	Asn	Pro	Asp	Arg	Ile
			260					265					270		
Lys	Thr	Asn	Arg	Lys	Ile	Phe	Thr	Leu	Ser	Thr	Glu	Asp	Phe	Glu	Ala
		275					280					285			
Ile	Asn	Asn	Ile	Ser	Lys	Glu	Lys	Gly	Glu	Lys	Arg	Val	Val	His	Pro
	290					295					300				
Asn	Trp	Ser	Pro	Phe	Glu	Val	Phe	Lys							
305					310										

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<210> 45
<211> 1029
<212> DNA
<213> Saccharomyces cerevisiae
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<400> 45
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60

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 acggaggcct ttggttaacaa cccaaaattc tccatggaag ttgtcccaga catatctaag 180
 ctggacgcat ttgaccatgt tttccaaaag cacggcaagg atatcaagat agttctacat 240
 acggcctctc cattctgctt tgatatcact gacagtgaac gcgatttatt aattcctgct 300
 gtgaacggtg ttaagggaaat tctccactca attaaaaaat acgccgctga ttctgtagaa 360
 cgtgtagttc tcacctcttc ttatgcagct gtgttcgata tggcaaaaga aaacgataag 420
 tctttaacat ttaacgaaga atcctggaac ccagctacct gggagagttg ccaaagtgac 480
 ccagttaacg cctactgtgg ttctaagaag ttgctgaaa aagcagcttg ggaatttcta 540
 gaggagaata gagactctgt aaaattcgaa ttaactgccg ttaaccctgt ttacgttttt 600
 ggtccgcaaa tgtttgacaa agatgtgaaa aaacacttga acacatcttg cgaactcgtc 660
 aacagcttga tgcatttatc accagaggac aagataccgg aactatttgg tggatacatt 720
 gatgttcgtg atgttgcaaa ggctcattta gttgccttcc aaaagaggga aacaattggt 780
 caaagactaa tcgtatcgga ggccagattt actatgcagg atgttctcga tctccttaac 840
 gaagacttcc ctgttctaaa aggcaatatt ccagtgggga aaccaggttc tggtgctacc 900
 cataacaccc ttggtgctac tcttgataat aaaaagagta agaaattggt aggtttcaag 960
 ttcaggaact tgaaagagac cattgacgac actgcctccc aaattttaaa atttgagggc 1020
 agaataataa 1029

<210> 46
 <211> 342
 <212> PRT
 <213> *Saccharomyces cerevisiae*
 <400> 46

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 Val Asp Leu Leu Leu Lys Glu Asp Tyr Lys Val Ile Gly Ser Ala Arg
 20 25 30
 Ser Gln Glu Lys Ala Glu Asn Leu Thr Glu Ala Phe Gly Asn Asn Pro
 35 40 45
 Lys Phe Ser Met Glu Val Val Pro Asp Ile Ser Lys Leu Asp Ala Phe
 50 55 60
 Asp His Val Phe Gln Lys His Gly Lys Asp Ile Lys Ile Val Leu His
 65 70 75 80
 Thr Ala Ser Pro Phe Cys Phe Asp Ile Thr Asp Ser Glu Arg Asp Leu
 85 90 95
 Leu Ile Pro Ala Val Asn Gly Val Lys Gly Ile Leu His Ser Ile Lys

cacactgcat ctccattctg ttttgacatc actgattctg agcgcgacct gctgattccg 300
gctgttaacg gtgttaaagg tattctgcac tctattaaga aatatgctgc tgattccgta 360
gaacgcgtag ttctgacttc ctcttatgct gcagtattcg atatggctaa agagaacgac 420
aaatccctga cttttaacga agaattcttg aaccgggcta cctgggaatc ttgccagtct 480
gacccgggta acgcttattg tggctctaag aagtttgctg aaaaagctgc ttgggaattc 540
ctggaagaaa accgtgactc tgtaaagttc gagctgaccg ctgtaaaccg ggtatacgtt 600
tttggcccgag agatgttcga taaagatgta aagaagcacc tgaacacttc ctgtgaactg 660
gtaaaactctc tgatgcacct gtctccagaa gataaaatcc cggagctgtt cggcgggttac 720
atcgacgttc gtgacgtagc aaaagcacat ctggtagctt tccagaagcg tgagactatc 780
ggccagcgtc tgattgtttc cgaggctcgt ttcacatgc aggatgttct ggatattctg 840
aacgaagact tcccgttact gaaaggtaac attccggtgg gtaaaccagg ctctggtgca 900
actcataaca ctctgggtgc aactctggat aacaagaagt ctaagaaact gctgggtttt 960
aaattccgta acctgaaaga aactattgac gacactgcat ctcagatcct gaaattcgaa 1020
ggtcgcatct aa 1032

<210> 48
<211> 343
<212> PRT
<213> Artificial Sequence

<400> 48

Met	Gly	Ser	Val	Phe	Val	Ser	Gly	Ala	Asn	Gly	Phe	Ile	Ala	Gln	His
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Ile	Val	Asp	Leu	Leu	Leu	Lys	Glu	Asp	Tyr	Lys	Val	Ile	Gly	Ser	Ala
			20					25					30		
Arg	Ser	Gln	Glu	Lys	Ala	Glu	Asn	Leu	Thr	Glu	Ala	Phe	Gly	Asn	Asn
		35					40					45			
Pro	Lys	Phe	Ser	Met	Glu	Val	Val	Pro	Asp	Ile	Ser	Lys	Leu	Asp	Ala
	50					55					60				
Phe	Asp	His	Val	Phe	Gln	Lys	His	Gly	Lys	Asp	Ile	Lys	Ile	Val	Leu
65					70				75						80
His	Thr	Ala	Ser	Pro	Phe	Cys	Phe	Asp	Ile	Thr	Asp	Ser	Glu	Arg	Asp
			85					90					95		
Leu	Leu	Ile	Pro	Ala	Val	Asn	Gly	Val	Lys	Gly	Ile	Leu	His	Ser	Ile
			100				105					110			
Lys	Lys	Tyr	Ala	Ala	Asp	Ser	Val	Glu	Arg	Val	Val	Leu	Thr	Ser	Ser
	115						120					125			
Tyr	Ala	Ala	Val	Phe	Asp	Met	Ala	Lys	Glu	Asn	Asp	Lys	Ser	Leu	Thr

130					135					140					
Phe 145	Asn	Glu	Glu	Ser	Trp 150	Asn	Pro	Ala	Thr	Trp 155	Glu	Ser	Cys	Gln	Ser 160
Asp	Pro	Val	Asn	Ala 165	Tyr	Cys	Gly	Ser	Lys 170	Lys	Phe	Ala	Glu	Lys 175	Ala
Ala	Trp	Glu	Phe 180	Leu	Glu	Glu	Asn	Arg 185	Asp	Ser	Val	Lys	Phe 190	Glu	Leu
Thr	Ala	Val 195	Asn	Pro	Val	Tyr	Val 200	Phe	Gly	Pro	Gln	Met 205	Phe	Asp	Lys
Asp	Val 210	Lys	Lys	His	Leu	Asn 215	Thr	Ser	Cys	Glu	Leu 220	Val	Asn	Ser	Leu
Met 225	His	Leu	Ser	Pro	Glu 230	Asp	Lys	Ile	Pro	Glu 235	Leu	Phe	Gly	Gly	Tyr 240
Ile	Asp	Val	Arg	Asp 245	Val	Ala	Lys	Ala	His 250	Leu	Val	Ala	Phe	Gln 255	Lys
Arg	Glu	Thr	Ile 260	Gly	Gln	Arg	Leu	Ile 265	Val	Ser	Glu	Ala	Arg 270	Phe	Thr
Met	Gln	Asp 275	Val	Leu	Asp	Ile	Leu 280	Asn	Glu	Asp	Phe	Pro 285	Val	Leu	Lys
Gly	Asn 290	Ile	Pro	Val	Gly	Lys 295	Pro	Gly	Ser	Gly	Ala 300	Thr	His	Asn	Thr
Leu 305	Gly	Ala	Thr	Leu	Asp 310	Asn	Lys	Lys	Ser	Lys 315	Lys	Leu	Leu	Gly	Phe 320
Lys	Phe	Arg	Asn	Leu 325	Lys	Glu	Thr	Ile	Asp 330	Asp	Thr	Ala	Ser	Gln 335	Ile
Leu	Lys	Phe	Glu 340	Gly	Arg	Ile									

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<210> 49
<211> 987
<212> DNA
<213> Artificial Sequence (isoleucine codon added)

<400> 49
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taccgtttat tcgatggtgc ttgcgactac ggcaacgaaa aggaagttgg tgaagggtatc 180
aggaaagcca tctccgaagg tcttgtttct agaaaggata tatttgttgt ttcaaagtta 240
tggaacaatt ttcaccatcc tgatcatgta aaattagctt taaagaagac cttaagcgat 300
atgggacttg attatttaga cctgtattat attcacttcc caatcgctt caaatatgtt 360
ccatttgaag agaaataccc tccaggattc tatacgggcg cagatgacga gaagaaaggt 420

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Leu	Ile	Gln	Asp	Leu	Leu	Arg	Gly	Cys	Arg	Ile	Lys	Pro	Val	Ala	Leu	
			180				185						190			
Gln	Ile	Glu	His	His	Pro	Tyr	Leu	Thr	Gln	Glu	His	Leu	Val	Glu	Phe	
			195				200						205			
Cys	Lys	Leu	His	Asp	Ile	Gln	Val	Val	Ala	Tyr	Ser	Ser	Phe	Gly	Pro	
		210				215					220					
Gln	Ser	Phe	Ile	Glu	Met	Asp	Leu	Gln	Leu	Ala	Lys	Thr	Thr	Pro	Thr	
		225				230					235		240			
Leu	Phe	Glu	Asn	Asp	Val	Ile	Lys	Lys	Val	Ser	Gln	Asn	His	Pro	Gly	
			245				250						255			
Ser	Thr	Thr	Ser	Gln	Val	Leu	Leu	Arg	Trp	Ala	Thr	Gln	Arg	Gly	Ile	
			260				265						270			
Ala	Val	Ile	Pro	Lys	Ser	Ser	Lys	Lys	Glu	Arg	Leu	Leu	Gly	Asn	Leu	
		275				280						285				
Glu	Ile	Glu	Lys	Lys	Phe	Thr	Leu	Thr	Glu	Gln	Glu	Leu	Lys	Asp	Ile	
		290				295					300					
Ser	Ala	Leu	Asn	Ala	Asn	Ile	Arg	Phe	Asn	Asp	Pro	Trp	Thr	Trp	Leu	
		305				310					315		320			
Asp	Gly	Lys	Phe	Pro	Thr	Phe	Ala									
				325												

<210>	51	
<211>	987	
<212>	DNA	
<213>	Artificial Sequence	
<400>	51	
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tatcgccctgt	tcgacggtgc	ttgcgactat ggtaacgaga aggaagttgg tgaaggcatc 180
cgtaaagcta	tctctgaagg	tctgggtatct cgtaaggata tctttgtagt atctaagctg 240
tggaacaact	ttcatcacc	ggatcacgta aaactggcac tgaagaaaac cctgtctgat 300
atgggtctgg	attatctgga	tctgtactat atccactttc cgatcgcat taaatacgta 360
cggttcgaag	aaaaatatcc	gccgggcttt tacactggtg cagacgacga aaagaagggt 420
cacatcactg	aagctcacgt	accgatcatc gacacttacc gtgctctgga ggaatgtgta 480
gacgaaggtc	tgatcaaata	tatcggtgta tctaacttcc agggttctct gatccaggat 540
ctgctgcgtg	gttgccgtat	caagccggtt gctctgcaaa ttgaacacca cccgtacctg 600
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tctttcggtc	cgcagtcctt	catcgaaatg gacctgcagc tggctaagac caccgact 720
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cagggtactgc tgcgttgggc tactcagcgt ggcacgcgtg ttatcccgaa atcttctaag 840
aaagaacgctc tgctgggtaa cctggaaatc gaaaagaaat tcactctgac cgaacaggaa 900
ctgaaagata tctctgctct gaacgctaac atccgtttca acgatccgtg gacctggctg 960
gatggtaaat tcccgaacttt cgcttaa 987

<210> 52
<211> 328
<212> PRT
<213> Artificial Sequence

<400> 52

Met Gly Ser Ser Leu Val Thr Leu Asn Asn Gly Leu Lys Met Pro Leu
1 5 10 15
Val Gly Leu Gly Cys Trp Lys Ile Asp Lys Lys Val Cys Ala Asn Gln
20 25 30
Ile Tyr Glu Ala Ile Lys Leu Gly Tyr Arg Leu Phe Asp Gly Ala Cys
35 40 45
Asp Tyr Gly Asn Glu Lys Glu Val Gly Glu Gly Ile Arg Lys Ala Ile
50 55 60
Ser Glu Gly Leu Val Ser Arg Lys Asp Ile Phe Val Val Ser Lys Leu
65 70 75 80
Trp Asn Asn Phe His His Pro Asp His Val Lys Leu Ala Leu Lys Lys
85 90 95
Thr Leu Ser Asp Met Gly Leu Asp Tyr Leu Asp Leu Tyr Tyr Ile His
100 105 110
Phe Pro Ile Ala Phe Lys Tyr Val Pro Phe Glu Glu Lys Tyr Pro Pro
115 120 125
Gly Phe Tyr Thr Gly Ala Asp Asp Glu Lys Lys Gly His Ile Thr Glu
130 135 140
Ala His Val Pro Ile Ile Asp Thr Tyr Arg Ala Leu Glu Glu Cys Val
145 150 155 160
Asp Glu Gly Leu Ile Lys Ser Ile Gly Val Ser Asn Phe Gln Gly Ser
165 170 175
Leu Ile Gln Asp Leu Leu Arg Gly Cys Arg Ile Lys Pro Val Ala Leu
180 185 190
Gln Ile Glu His His Pro Tyr Leu Thr Gln Glu His Leu Val Glu Phe
195 200 205
Cys Lys Leu His Asp Ile Gln Val Val Ala Tyr Ser Ser Phe Gly Pro
210 215 220
Gln Ser Phe Ile Glu Met Asp Leu Gln Leu Ala Lys Thr Thr Pro Thr
225 230 235 240

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<210> 55
<211> 1464
<212> DNA
<213> Artificial Sequence
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gtagaaaaga tcatcatgcc aggtgtaacc cactggcact ctccgtactt tttcgcatat	240
ttcccgactg catcctccta cccggctatg ctggctgaca tgctgtgtgg tgctatcggc	300
tgtatcggct tttcctgggc tgcattctccg gcatgcactg agctggaaac cgttatgatg	360
gattggctgg gtaaaatgct gcagctgccg gaggcatttc tggctgggtga ggctgggtgag	420
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ctgattgggtg gtgttaagct gaaagctatt ccgtccgatg gtaagttcgc tatgcgtgca	660
tccgctctgc aagaagctct ggaacgtgac aaagctgctg gtctgattcc gttcttcgtt	720
gttgctaccc tgggtactac ctcttgctgt tctttcgaca acctgctgga agttgggtccg	780
atctgtcacg aggaggacat ctggctgcac gttgacgcag catatgctgg ctctgctttt	840
atctgtccgg aattccgtca cctgctgaac ggcgttgagt tcgctgattc tttcaacttc	900
aaccgcaca agtggctgct ggtaactttt gattgctcgg ctatgtgggt aaaacgtcgc	960
actgatctga ccggtgcatt taaactggac ccggtatatc tgaagcattc tcaccagggt	1020
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gtttgcgctg aagttaccct gggcctgggt tgcttccgtc tgaagggttc tgatggctctg	1260
aacgaagctc tgctggagcg tattaactcg gctcgtaaaa tccacctggt tccgtgtcgt	1320
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<210> 56
 <211> 487
 <212> PRT
 <213> Artificial Sequence

<400> 56

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-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20							25					30				
Asp	Val	Gln	Pro	Gly	Tyr	Leu	Arg	Pro	Leu	Ile	Pro	Ala	Thr	Ala	Pro	
		35					40					45				
Gln	Glu	Pro	Asp	Thr	Phe	Glu	Asp	Ile	Leu	Gln	Asp	Val	Glu	Lys	Ile	
	50					55					60					
Ile	Met	Pro	Gly	Val	Thr	His	Trp	His	Ser	Pro	Tyr	Phe	Phè	Ala	Tyr	
65					70					75					80	
Phe	Pro	Thr	Ala	Ser	Ser	Tyr	Pro	Ala	Met	Leu	Ala	Asp	Met	Leu	Cys	
				85					90					95		
Gly	Ala	Ile	Gly	Cys	Ile	Gly	Phe	Ser	Trp	Ala	Ala	Ser	Pro	Ala	Cys	
			100					105					110			
Thr	Glu	Leu	Glu	Thr	Val	Met	Met	Asp	Trp	Leu	Gly	Lys	Met	Leu	Gln	
		115					120					125				
Leu	Pro	Glu	Ala	Phe	Leu	Ala	Gly	Glu	Ala	Gly	Glu	Gly	Gly	Gly	Val	
	130					135					140					
Ile	Gln	Gly	Ser	Ala	Ser	Glu	Ala	Thr	Leu	Val	Ala	Leu	Leu	Ala	Ala	
145					150					155					160	
Arg	Thr	Lys	Val	Val	Arg	Arg	Leu	Gln	Ala	Ala	Ser	Pro	Gly	Leu	Thr	
				165					170					175		
Gln	Gly	Ala	Val	Leu	Glu	Lys	Leu	Val	Ala	Tyr	Ala	Ser	Asp	Gln	Ala	
			180						185				190			
His	Ser	Ser	Val	Glu	Arg	Ala	Gly	Leu	Ile	Gly	Gly	Val	Lys	Leu	Lys	
		195					200					205				
Ala	Ile	Pro	Ser	Asp	Gly	Lys	Phe	Ala	Met	Arg	Ala	Ser	Ala	Leu	Gln	
	210					215					220					
Glu	Ala	Leu	Glu	Arg	Asp	Lys	Ala	Ala	Gly	Leu	Ile	Pro	Phe	Phe	Val	
225					230					235					240	
Val	Ala	Thr	Leu	Gly	Thr	Thr	Ser	Cys	Cys	Ser	Phe	Asp	Asn	Leu	Leu	
				245					250					255		
Glu	Val	Gly	Pro	Ile	Cys	His	Glu	Glu	Asp	Ile	Trp	Leu	His	Val	Asp	
			260					265					270			
Ala	Ala	Tyr	Ala	Gly	Ser	Ala	Phe	Ile	Cys	Pro	Glu	Phe	Arg	His	Leu	
		275					280					285				
Leu	Asn	Gly	Val	Glu	Phe	Ala	Asp	Ser	Phe	Asn	Phe	Asn	Pro	His	Lys	
	290					295					300					
Trp	Leu	Leu	Val	Asn	Phe	Asp	Cys	Ser	Ala	Met	Trp	Val	Lys	Arg	Arg	
305					310					315					320	
Thr	Asp	Leu	Thr	Gly	Ala	Phe	Lys	Leu	Asp	Pro	Val	Tyr	Leu	Lys	His	
				325					330					335		
Ser	His	Gln	Gly	Ser	Gly	Leu	Ile	Thr	Asp	Tyr	Arg	His	Trp	Gln	Leu	
			340					345					350			

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 aataaatatg gtgctggtaa tgccatgact cctcactact ctggtactac tttagacgct 960
 caaacaagat acgctgaagg tactaaaaat attttgaat cattctttac cggtaaattt 1020
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 aaacacgata agaaataa 1098

<210> 58
 <211> 365
 <212> PRT
 <213> *Candida boidinii*

<400> 58

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Asp	Glu	Glu	Lys	Leu	Tyr	Gly	Cys	Thr	Glu	Asn	Lys	Leu	Gly	Ile	Ala	20	25	30	
Asn	Trp	Leu	Lys	Asp	Gln	Gly	His	Glu	Leu	Ile	Thr	Thr	Ser	Asp	Lys	35	40	45	
Glu	Gly	Glu	Thr	Ser	Glu	Leu	Asp	Lys	His	Ile	Pro	Asp	Ala	Asp	Ile	50	55	60	
Ile	Ile	Thr	Thr	Pro	Phe	His	Pro	Ala	Tyr	Ile	Thr	Lys	Glu	Arg	Leu	65	70	75	80
Asp	Lys	Ala	Lys	Asn	Leu	Lys	Leu	Val	Val	Val	Ala	Gly	Val	Gly	Ser	85	90	95	
Asp	His	Ile	Asp	Leu	Asp	Tyr	Ile	Asn	Gln	Thr	Gly	Lys	Lys	Ile	Ser	100	105	110	
Val	Leu	Glu	Val	Thr	Gly	Ser	Asn	Val	Val	Ser	Val	Ala	Glu	His	Val	115	120	125	
Val	Met	Thr	Met	Leu	Val	Leu	Val	Arg	Asn	Phe	Val	Pro	Ala	His	Glu	130	135	140	
Gln	Ile	Ile	Asn	His	Asp	Trp	Glu	Val	Ala	Ala	Ile	Ala	Lys	Asp	Ala	145	150	155	160
Tyr	Asp	Ile	Glu	Gly	Lys	Thr	Ile	Ala	Thr	Ile	Gly	Ala	Gly	Arg	Ile	165	170	175	
Gly	Tyr	Arg	Val	Leu	Glu	Arg	Leu	Leu	Pro	Phe	Asn	Pro	Lys	Glu	Leu	180	185	190	
Leu	Tyr	Tyr	Asp	Tyr	Gln	Ala	Leu	Pro	Lys	Glu	Ala	Glu	Glu	Lys	Val	195	200	205	
Gly	Ala	Arg	Arg	Val	Glu	Asn	Ile	Glu	Glu	Leu	Val	Ala	Gln	Ala	Asp	210	215	220	

Ile Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile
 225 230 235 240
 Asn Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Val Asn
 245 250 255
 Thr Ala Arg Gly Ala Ile Cys Val Ala Glu Asp Val Ala Ala Leu
 260 265 270
 Glu Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln
 275 280 285
 Pro Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly
 290 295 300
 Ala Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala
 305 310 315 320
 Gln Thr Arg Tyr Ala Glu Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe
 325 330 335
 Thr Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly
 340 345 350
 Glu Tyr Val Thr Lys Ala Tyr Gly Lys His Asp Lys Lys
 355 360 365

<210> 59
 <211> 1098
 <212> DNA
 <213> Artificial Sequence

<400> 59
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 gaactgatca ctacctctga caaagaaggt gaaacctctg aactggacaa acacatcccg 180
 gatgcagata tcatcatcac cactccgttc caccggctt acatcaccaa agagcgtctg 240
 gacaaagcta aaaacctgaa actggtagta gttgctggtg taggttctga ccacatcgac 300
 ctggactaca tcaaccagac tggtaaaaaa atctctgtac tggaagtaac tggttctaac 360
 gttgtttctg ttgctgaaca cgttgtaatg actatgctgg ttctgggtcg taacttcggt 420
 ccggctcacg aacagatcat caaccagat tgggaagttg cagcaatcg taaagacgct 480
 tatgacatcg aaggcaaaac catcgctact atcggcgtg gccgtatcgg ttaccgtggt 540
 ctggaacgtc tgctgccgtt caaccgaaa gaactgctgt actacgacta ccaggctctg 600
 ccgaaagaag cagaggagaa agttggtgct cgccgtgtag agaacatcga agagctggta 660
 gctcaggctg acatcgttac tgtaaacgt cgcgtgcacg caggcactaa aggtctgatt 720
 aacaaagagc tgctgtctaa attcaaaaaa ggtgcatggc tggttaacac tgcacgtggt 780
 gctatctgcg ttgctgaaga cgttgctgct gcaactggaat ctggtcagct gcgtgggttac 840

225		230		235		240
Asn Lys Glu Leu	Leu Ser Lys Phe Lys	Lys Gly Ala Trp Leu	Val Asn			
	245	250	255			
Thr Ala Arg Gly	Ala Ile Cys Val	Ala Glu Asp Val	Ala Ala Leu			
	260	265	270			
Glu Ser Gly Gln	Leu Arg Gly Tyr	Gly Gly Asp Val	Trp Phe Pro Gln			
	275	280	285			
Pro Ala Pro Lys	Asp His Pro Trp	Arg Asp Met Arg	Asn Lys Tyr Gly			
	290	295	300			
Ala Gly Asn Ala	Met Thr Pro His	Tyr Ser Gly Thr	Thr Leu Asp Ala			
305	310	315	320			
Gln Thr Arg Tyr	Ala Glu Gly Thr	Lys Asn Ile Leu	Glu Ser Phe Phe			
	325	330	335			
Thr Gly Lys Phe	Asp Tyr Arg Pro	Gln Asp Ile Ile	Leu Leu Asn Gly			
	340	345	350			
Glu Tyr Val Thr	Lys Ala Tyr Gly	Lys His Asp Lys	Lys			
	355	360	365			

<210> 61
 <211> 1488
 <212> DNA
 <213> Pseudomonas putida

<400> 61
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 cacatgcagt tgccattcat gggcaccgtg gccagcgagg atttcttcag cggcaccgca 240
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 ggcatgaccg gaccagaggc tcacccctt tcgcgcctt cacaagtggg aggtgaagcg 660
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 tccagccgtg aagcactgga tgaaatcacc tatgcacgcg ccaagggcca gccggtttac 780
 ggcgaagtct tgcccggcca cctgctgctg gacgacagcg tctaccgtga cccggactgg 840
 gccactgccg ctggctacgt gatgagcccc ccgttccgcc cgcgcgagca ccaggaggcg 900

Gly	Ala	Val	Pro	Thr	Val	His	Ala	Glu	Asn	Gly	Glu	Leu	Val	Tyr	His
180			185			190									
Leu	Gln	Lys	Lys	Leu	Leu	Ala	Gln	Gly	Met	Thr	Gly	Pro	Glu	Ala	His
195			200			205									
Pro	Leu	Ser	Arg	Pro	Ser	Gln	Val	Glu	Gly	Glu	Ala	Ala	Ser	Arg	Ala
210			215			220									
Ile	Arg	Ile	Ala	Glu	Thr	Ile	Gly	Thr	Pro	Leu	Tyr	Val	Val	His	Ile
225			230			235									
Ser	Ser	Arg	Glu	Ala	Leu	Asp	Glu	Ile	Thr	Tyr	Ala	Arg	Ala	Lys	Gly
245			250			255									
Gln	Pro	Val	Tyr	Gly	Glu	Val	Leu	Pro	Gly	His	Leu	Leu	Leu	Asp	Asp
260			265			270									
Ser	Val	Tyr	Arg	Asp	Pro	Asp	Trp	Ala	Thr	Ala	Ala	Gly	Tyr	Val	Met
275			280			285									
Ser	Pro	Pro	Phe	Arg	Pro	Arg	Glu	His	Gln	Glu	Ala	Leu	Trp	Arg	Gly
290			295			300									
Leu	Gln	Ser	Gly	Asn	Leu	His	Thr	Thr	Ala	Thr	Asp	His	Cys	Cys	Phe
305			310			315									
Cys	Ala	Glu	Gln	Lys	Ala	Met	Gly	Arg	Asp	Asp	Phe	Ser	Arg	Ile	Pro
325			330			335									
Asn	Gly	Thr	Ala	Gly	Ile	Glu	Asp	Arg	Met	Ala	Val	Leu	Trp	Asp	Ala
340			345			350									
Gly	Val	Asn	Ser	Gly	Arg	Leu	Ser	Met	His	Glu	Phe	Val	Ala	Leu	Thr
355			360			365									
Ser	Thr	Asn	Thr	Ala	Lys	Ile	Phe	Asn	Leu	Phe	Pro	Arg	Lys	Gly	Ala
370			375			380									
Ile	Arg	Val	Gly	Ala	Asp	Ala	Asp	Leu	Val	Leu	Trp	Asp	Pro	Gln	Gly
385			390			395									
Thr	Arg	Thr	Leu	Ser	Ala	Gln	Thr	His	His	Gln	Arg	Val	Asp	Phe	Asn
405			410			415									
Ile	Phe	Glu	Gly	Arg	Thr	Val	Arg	Gly	Val	Pro	Ser	His	Thr	Ile	Ser
420			425			430									
Gln	Gly	Lys	Val	Leu	Trp	Ala	Asp	Gly	Asp	Leu	Arg	Arg	Arg	Gly	Arg
435			440			445									
Gly	Gly	Ala	Val	Cys	Gly	Thr	Ala	Gly	Val	Ser	Val	Gly	Val	Arg	Gly
450			455			460									
Ala	Gly	Ala	Thr	Arg	Arg	Thr	Ala	Ala	Pro	Asp	Ala	Arg	Ser	Ala	Leu
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Arg	Pro	Leu	Gly	Leu	Leu	Arg	Ser	Pro	Ser	Pro	Ala	Ser	Gln	Ile	
485			490			495									

<210> 63
 <211> 1491
 <212> DNA
 <213> Artificial Sequence

<400> 63
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 cagtctctgc tggaagcttt ccatacttgg cgtggttggg ctcagaaatc tgcattctgac 360
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 tacgggtgaag ttctgccggg tcattctgtg ctggatgatt ctgtataccg cgatccggac 840
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 gctggcattg aggaccgtat ggctgttctg tgggatgctg gcgttaactc tggctcgtctg 1080
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 gacggtgacc tgcgtcgtcg tggctcgtgg ggtgctgttt gcggtaccgc tgggtgttct 1380
 gttggtgttc gtggcgctgg tgctaccgct cgtactgctg ctccggatgc tcgttctgct 1440
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<210> 64
 <211> 496
 <212> PRT
 <213> Artificial Sequence

[illegible]

44


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attgttacca agatcgggat ctggttaatg cccaatccag ggggttatca atcctacttg 840
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gagccgattc gaagggttct ctgggaaacg attaaagacg cattctcggc gatcccaggc 1140
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<210> 66
<211> 560
<212> PRT
<213> Penicillium simplicissimum

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<400> 66

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20          25          30
Gly Ser Glu Asn Val Glu Val Ile Ser Ser Lys Asp Gln Ile Val Asp
35          40          45
Gly Ser Tyr Met Lys Pro Thr His Thr His Asp Pro His His Val Met
50          55          60
Asp Gln Asp Tyr Phe Leu Ala Ser Ala Ile Val Ala Pro Arg Asn Val
65          70          75          80

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003027 424260

Ala	Asp	Val	Gln	Ser	Ile	Val	Gly	Leu	Ala	Asn	Lys	Phe	Ser	Phe	Pro	85	90	95
Leu	Trp	Pro	Ile	Ser	Ile	Gly	Arg	Asn	Ser	Gly	Tyr	Gly	Gly	Ala	Ala	100	105	110
Pro	Arg	Val	Ser	Gly	Ser	Val	Val	Leu	Asp	Met	Gly	Lys	Asn	Met	Asn	115	120	125
Arg	Val	Leu	Glu	Val	Asn	Val	Glu	Gly	Ala	Tyr	Cys	Val	Val	Glu	Pro	130	135	140
Gly	Val	Thr	Tyr	His	Asp	Leu	His	Asn	Tyr	Leu	Glu	Ala	Asn	Asn	Leu	145	150	155
Arg	Asp	Lys	Leu	Trp	Leu	Asp	Val	Pro	Asp	Leu	Gly	Gly	Gly	Ser	Val	165	170	175
Leu	Gly	Asn	Ala	Val	Glu	Arg	Gly	Val	Gly	Tyr	Thr	Pro	Tyr	Gly	Asp	180	185	190
His	Trp	Met	Met	His	Ser	Gly	Met	Glu	Val	Val	Leu	Ala	Asn	Gly	Glu	195	200	205
Leu	Leu	Arg	Thr	Gly	Met	Gly	Ala	Leu	Pro	Asp	Pro	Lys	Arg	Pro	Glu	210	215	220
Thr	Met	Gly	Leu	Lys	Pro	Glu	Asp	Gln	Pro	Trp	Ser	Lys	Ile	Ala	His	225	230	235
Leu	Phe	Pro	Tyr	Gly	Phe	Gly	Pro	Tyr	Ile	Asp	Gly	Leu	Phe	Ser	Gln	245	250	255
Ser	Asn	Met	Gly	Ile	Val	Thr	Lys	Ile	Gly	Ile	Trp	Leu	Met	Pro	Asn	260	265	270
Pro	Gly	Gly	Tyr	Gln	Ser	Tyr	Leu	Ile	Thr	Leu	Pro	Lys	Asp	Gly	Asp	275	280	285
Leu	Lys	Gln	Ala	Val	Asp	Ile	Ile	Arg	Pro	Leu	Arg	Leu	Gly	Met	Ala	290	295	300
Leu	Gln	Asn	Val	Pro	Thr	Ile	Arg	His	Ile	Leu	Leu	Asp	Ala	Ala	Val	305	310	315
Leu	Gly	Asp	Lys	Arg	Ser	Tyr	Ser	Ser	Lys	Thr	Glu	Pro	Leu	Ser	Asp	325	330	335
Glu	Glu	Leu	Asp	Lys	Ile	Ala	Lys	Gln	Leu	Asn	Leu	Gly	Arg	Trp	Asn	340	345	350
Phe	Tyr	Gly	Ala	Leu	Tyr	Gly	Pro	Glu	Pro	Ile	Arg	Arg	Val	Leu	Trp	355	360	365
Glu	Thr	Ile	Lys	Asp	Ala	Phe	Ser	Ala	Ile	Pro	Gly	Val	Lys	Phe	Tyr	370	375	380
Phe	Pro	Glu	Asp	Thr	Pro	Glu	Asn	Ser	Val	Leu	Arg	Val	Arg	Asp	Lys	385	390	395
Thr	Met	Gln	Gly	Ile	Pro	Thr	Tyr	Asp	Glu	Leu	Lys	Trp	Ile	Asp	Trp			

415

Lys Ser Gly Val Trp Pro Ser Gln Tyr Ser His Val Thr Trp Lys Leu
545 550 555 560

<213> Artificial Sequence

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		115					120					125			
Asn	Arg	Val	Leu	Glu	Val	Asn	Val	Glu	Gly	Ala	Tyr	Cys	Val	Val	Glu
	130					135					140				
Pro	Gly	Val	Thr	Tyr	His	Asp	Leu	His	Asn	Tyr	Leu	Glu	Ala	Asn	Asn
145					150					155					160
Leu	Arg	Asp	Lys	Leu	Trp	Leu	Asp	Val	Pro	Asp	Leu	Gly	Gly	Gly	Ser
				165					170					175	
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			180					185					190		
Asp	His	Trp	Met	Met	His	Ser	Gly	Met	Glu	Val	Val	Leu	Ala	Asn	Gly
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Glu	Leu	Leu	Arg	Thr	Gly	Met	Gly	Ala	Leu	Pro	Asp	Pro	Lys	Arg	Pro
	210					215					220				
Glu	Thr	Met	Gly	Leu	Lys	Pro	Glu	Asp	Gln	Pro	Trp	Ser	Lys	Ile	Ala
225					230					235					240
His	Leu	Phe	Pro	Tyr	Gly	Phe	Gly	Pro	Tyr	Ile	Asp	Gly	Leu	Phe	Ser
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Gln	Ser	Asn	Met	Gly	Ile	Val	Thr	Lys	Ile	Gly	Ile	Trp	Leu	Met	Pro
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Asn	Pro	Gly	Gly	Tyr	Gln	Ser	Tyr	Leu	Ile	Thr	Leu	Pro	Lys	Asp	Gly
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Asp	Leu	Lys	Gln	Ala	Val	Asp	Ile	Ile	Arg	Pro	Leu	Arg	Leu	Gly	Met
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Ala	Leu	Gln	Asn	Val	Pro	Thr	Ile	Arg	His	Ile	Leu	Leu	Asp	Ala	Ala
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Val	Leu	Gly	Asp	Lys	Arg	Ser	Tyr	Ser	Ser	Lys	Thr	Glu	Pro	Leu	Ser
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			340					345					350		
Asn	Phe	Tyr	Gly	Ala	Leu	Tyr	Gly	Pro	Glu	Pro	Ile	Arg	Arg	Val	Leu
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Trp	Glu	Thr	Ile	Lys	Asp	Ala	Phe	Ser	Ala	Ile	Pro	Gly	Val	Lys	Phe
	370					375					380				
Tyr	Phe	Pro	Glu	Asp	Thr	Pro	Glu	Asn	Ser	Val	Leu	Arg	Val	Arg	Asp
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Lys	Thr	Met	Gln	Gly	Ile	Pro	Thr	Tyr	Asp	Glu	Leu	Lys	Trp	Ile	Asp
				405					410					415	
Trp	Leu	Pro	Asn	Gly	Ala	His	Leu	Phe	Phe	Ser	Pro	Ile	Ala	Lys	Val
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445

Leu

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<210> 70
 <211> 283
 <212> PRT
 <213> Candida magnoliae

<400> 70

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Gly	Lys	Val	Ala	Ser	Ile	Thr	Gly	Ser	Ser	Ser	Gly	Ile	Gly	Tyr	Ala	
		35					40					45				
Leu	Ala	Glu	Ala	Phe	Ala	Gln	Val	Gly	Ala	Asp	Val	Ala	Ile	Trp	Tyr	
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Asn	Ser	His	Asp	Ala	Thr	Gly	Lys	Ala	Glu	Ala	Leu	Ala	Lys	Lys	Tyr	
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Gly	Val	Lys	Val	Lys	Ala	Tyr	Lys	Ala	Asn	Val	Ser	Ser	Ser	Asp	Ala	
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Val	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile	Lys	Asp	Phe	Gly	His	Leu	Asp	
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Ile	Val	Val	Ala	Asn	Ala	Gly	Ile	Pro	Trp	Thr	Lys	Gly	Ala	Tyr	Ile	
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Lys	Gly	Val	Gly	Tyr	Val	Ala	Lys	His	Ala	Gly	Arg	His	Phe	Arg	Glu	
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			180					185					190			
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Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly	
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Ala	Tyr	Leu	Phe	Leu	Ala	Ser	Asp	Ala	Gly	Ser	Tyr	Ala	Thr	Gly	Thr	
			260					265					270			
Asp	Ile	Ile	Val	Asp	Gly	Gly	Tyr	Thr	Leu	Pro						

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 <211> 533
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 73

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			20					25					30		
Glu	Asn	Ala	Val	Val	Thr	Lys	Thr	Ala	Ser	Gly	Arg	Phe	Asp	Val	Thr
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Pro	Thr	Val	Gln	Asp	Tyr	Val	Phe	Lys	Leu	Asp	Leu	Lys	Lys	Pro	Glu
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Lys	Leu	Gly	Ile	Met	Leu	Ile	Gly	Leu	Gly	Gly	Asn	Asn	Gly	Ser	Thr
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Leu	Val	Ala	Ser	Val	Leu	Ala	Asn	Lys	His	Asn	Val	Glu	Phe	Gln	Thr	
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Lys	Glu	Gly	Val	Lys	Gln	Pro	Asn	Tyr	Phe	Gly	Ser	Met	Thr	Gln	Cys	
				100					105					110		
Ser	Thr	Leu	Lys	Leu	Gly	Ile	Asp	Ala	Glu	Gly	Asn	Asp	Val	Tyr	Ala	
				115					120					125		
Pro	Phe	Asn	Ser	Leu	Leu	Pro	Met	Val	Ser	Pro	Asn	Asp	Phe	Val	Val	
				130					135					140		
Ser	Gly	Trp	Asp	Ile	Asn	Asn	Ala	Asp	Leu	Tyr	Glu	Ala	Met	Gln	Arg	
				145					150					155		
Ser	Gln	Val	Leu	Glu	Tyr	Asp	Leu	Gln	Gln	Arg	Leu	Lys	Ala	Lys	Met	
				165					170					175		
Ser	Leu	Val	Lys	Pro	Leu	Pro	Ser	Ile	Tyr	Tyr	Pro	Asp	Phe	Ile	Ala	
				180					185					190		
Ala	Asn	Gln	Asp	Glu	Arg	Ala	Asn	Asn	Cys	Ile	Asn	Leu	Asp	Glu	Lys	
				195					200					205		
Gly	Asn	Val	Thr	Thr	Arg	Gly	Lys	Trp	Thr	His	Leu	Gln	Arg	Ile	Arg	
				210					215					220		
Arg	Asp	Ile	Gln	Asn	Phe	Lys	Glu	Glu	Asn	Ala	Leu	Asp	Lys	Val	Ile	
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				245					250					255		
Val	Asn	Asp	Thr	Met	Glu	Asn	Leu	Leu	Gln	Ser	Ile	Lys	Asn	Asp	His	
				260					265					270		
Glu	Glu	Ile	Ala	Pro	Ser	Thr	Ile	Phe	Ala	Ala	Ala	Ser	Ile	Leu	Glu	
				275					280					285		
Gly	Val	Pro	Tyr	Ile	Asn	Gly	Ser	Pro	Gln	Asn	Thr	Phe	Val	Pro	Gly	
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Leu	Val	Gln	Leu	Ala	Glu	His	Glu	Gly	Thr	Phe	Ile	Ala	Gly	Asp	Asp	
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Leu	Lys	Ser	Gly	Gln	Thr	Lys	Leu	Lys	Ser	Val	Leu	Ala	Gln	Phe	Leu	
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Val	Asp	Ala	Gly	Ile	Lys	Pro	Val	Ser	Ile	Ala	Ser	Tyr	Asn	His	Leu	
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Lys	Glu	Ile	Ser	Lys	Ser	Ser	Val	Ile	Asp	Asp	Ile	Ile	Ala	Ser	Asn	
				370					375					380		
Asp	Ile	Leu	Tyr	Asn	Asp	Lys	Leu	Gly	Lys	Lys	Val	Asp	His	Cys	Ile	
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<211> 1605
<212> DNA
<213> Artificial Sequence
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<210> 75
<211> 534
<212> PRT
<213> Artificial Sequence

<400> 75

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Tyr	Glu	Asn	Ala	Val	Val	Thr	Lys	Thr	Ala	Ser	Gly	Arg	Phe	Asp	Val	35	40	45	
Thr	Pro	Thr	Val	Gln	Asp	Tyr	Val	Phe	Lys	Leu	Asp	Leu	Lys	Lys	Pro	50	55	60	
Glu	Lys	Leu	Gly	Ile	Met	Leu	Ile	Gly	Leu	Gly	Gly	Asn	Asn	Gly	Ser	65	70	75	80
Thr	Leu	Val	Ala	Ser	Val	Leu	Ala	Asn	Lys	His	Asn	Val	Glu	Phe	Gln	85	90	95	
Thr	Lys	Glu	Gly	Val	Lys	Gln	Pro	Asn	Tyr	Phe	Gly	Ser	Met	Thr	Gln	100	105	110	
Cys	Ser	Thr	Leu	Lys	Leu	Gly	Ile	Asp	Ala	Glu	Gly	Asn	Asp	Val	Tyr	115	120	125	
Ala	Pro	Phe	Asn	Ser	Leu	Leu	Pro	Met	Val	Ser	Pro	Asn	Asp	Phe	Val	130	135	140	
Val	Ser	Gly	Trp	Asp	Ile	Asn	Asn	Ala	Asp	Leu	Tyr	Glu	Ala	Met	Gln				

Val Leu Thr Phe Leu Ser Tyr Trp Leu Lys Ala Pro Leu Thr Arg Pro
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Gly Phe His Pro Val Asn Gly Leu Asn Lys Gln Arg Thr Ala Leu Glu
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Asn Phe Leu Arg Leu Leu Ile Gly Leu Pro Ser Gln Asn Glu Leu Arg
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Phe Glu Glu Arg Leu Leu
530

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<210> 76
<211> 2043
<212> DNA
<213> Hypomyces rosellus
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<210> 77
 <211> 680
 <212> PRT
 <213> Hypomyces rosellus

<400> 77

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			20					25					30		
Gly	Ser	Leu	Gln	Phe	Leu	Ser	Leu	Arg	Ala	Ser	Ala	Pro	Ile	Gly	Ser
		35					40					45			
Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val	Thr	Cys	Asp	Ser	Ala	Gln	Ser
	50					55					60				
Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp	Gly	Asn	Lys	Asp	Thr	Phe	Trp
65				70					75					80	
His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp	Pro	Lys	Pro	Pro	His	Thr	Tyr
				85				90						95	
Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn	Val	Asn	Gly	Leu	Ser	Met	Leu
			100					105					110		
Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly	Trp	Ile	Gly	Arg	His	Glu	Val
		115					120					125			
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Pro Ala Arg Tyr Val 165	Arg Leu Val Ala Ile 170	Thr Glu Ala Asn Gly Gln 175
Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Gln Ala Ser Ser Tyr 180 185 190		
Thr Ala Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Ile Asp Leu 195 200 205		
Pro Ile Val Pro Ala Ala Ala Ala Ile Glu Pro Thr Ser Gly Arg Val 210 215 220		
Leu Met Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly 225 230 235 240		
Gly Ile Thr Leu Thr Ser Ser Trp Asp Pro Ser Thr Gly Ile Val Ser 245 250 255		
Asp Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile 260 265 270		
Ser Met Asp Gly Asn Gly Gln Ile Val Val Thr Gly Gly Asn Asp Ala 275 280 285		
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Glu Lys Asn Gly Glu Val Tyr Ser Pro Ser Ser Lys Thr Trp Thr Ser 340 345 350		
Leu Pro Asn Ala Lys Val Asn Pro Met Leu Thr Ala Asp Lys Gln Gly 355 360 365		
Leu Tyr Arg Ser Asp Asn His Ala Trp Leu Phe Gly Trp Lys Lys Gly 370 375 380		
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Ser Gly Ser Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Asn Arg 405 410 415		
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Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Asp Tyr Gln Asp 435 440 445		
Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Leu Gly Glu Pro Gly 450 455 460		

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Glu	Gly	Ser	Leu	Gln	Phe	Leu	Ser	Leu	Arg	Ala	Ser	Ala	Pro	Ile	Gly
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Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp	Pro	Lys	Pro	Pro	His	Thr
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Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp	Gly	Ser	Pro	Val	Ala	Ser
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Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys	Tyr	Ser	Asn	Phe	Glu	Thr
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Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala	Ile	Thr	Glu	Ala	Asn	Gly
				165					170					175	
Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn	Val	Phe	Gln	Ala	Ser	Ser
			180					185					190		
Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg	Trp	Gly	Pro	Thr	Ile	Asp
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Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile	Glu	Pro	Thr	Ser	Gly	Arg
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Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp	Ala	Phe	Gly	Gly	Ser	Pro
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Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp	Pro	Ser	Thr	Gly	Ile	Val
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Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser	Ser	Asp	Ser	Trp	Ile	Pro
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Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu	Thr	Leu	Thr	Asn	Asn	Gly
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Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn	Ser	Ala	Gly	Val	Pro	Ser
			660					665					670		
Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln							
		675					680								

09/11/15 15:00